

First complete genome sequence of the Zika virus

January 11 2016



An *Aedes aegypti* mosquito. Credit: Institut Pasteur

Having confirmed the first cases of infection in Suriname then in French Guiana, the Institut Pasteur in French Guiana has sequenced the

complete genome of the Zika virus, which is responsible for an unprecedented epidemic currently sweeping through the tropical regions of the Americas. Published in *The Lancet* medical journal, the analysis of this sequence shows almost complete homology with the strains responsible for the epidemic that occurred in the Pacific in 2013 and 2014.

Last November, following a request by colleagues in Suriname, the team from the Virology Laboratory at the Institut Pasteur in French Guiana—a National Reference Center for Arboviruses for the Antilles-French Guiana region—confirmed the first five indigenous cases of infection by the Zika [virus](#) in Suriname. Researchers from the Institut Pasteur in French Guiana have just mapped the [complete genome sequence](#) of this [viral strain](#) using one of these five samples. The analysis of this genome, which features in *The Lancet* today, shows that it belongs to the Asian lineage and presents over 99% homology with the strain responsible for the epidemic in French Polynesia in 2013. "Until now few complete sequences of this virus and none of the strains currently circulating in South and Central America were available. This complete sequence of the virus is a major starting point for shedding light on how its behavior develops", points out Dominique Rousset, Head of the Virology Laboratory and National Reference Center for Arboviruses at the Institut Pasteur in French Guiana.

The first cases were confirmed in Brazil in May 2015 and the country is currently experiencing the largest epidemic ever recorded with 440,000 to 1,300,000 suspected cases reported by the Brazilian health authorities. The Zika virus has spread quickly, affecting 10 countries in the [tropical regions](#) of the Americas as well as the Caribbean so far. While until recently the infection was considered harmless, the Zika virus epidemic which raged in French Polynesia and the Pacific in 2013-2014 was accompanied by an increase in serious neurological complications, such as Guillain-Barre syndrome and congenital neurological defects. In

Brazil, the very significant increase in the number of microcephaly cases in fetuses whose mothers were infected during pregnancy forced the government to declare a state of emergency in December 2015. "Are these defects caused by the Zika virus alone, the co-circulation of other infectious agents or other factors? Multidisciplinary research projects will need to be set up to answer these questions. We are already trying to improve our knowledge of this virus and understand its development, primarily by building on diagnostic tools" explains Dominique Rousset.

In addition, a team of four researchers from the Institut Pasteur in Dakar arrived in Sao Paulo on January 5th, to help Brazilian scientists deal with the Zika epidemic.

To date, 17 cases have been confirmed in French Guiana and three in Martinique. Given the very rapid spread of the Zika virus, the Institut Pasteur in French Guiana remains actively involved in epidemiological monitoring, alongside the health authorities and the Institut Pasteur International Network. "We are committed to supporting vector control by monitoring resistance to insecticides, as part of an agreement with the Regional Health Agency. Research into the impact of this resistance on the vectorial competence of *Aedes aegypti* populations for various arboviruses, including the Zika virus, is also being conducted at the Vectopole", adds Isabelle Dusfour, entomologist at the Institut Pasteur in French Guiana.

Described for the first time in Uganda in 1947, Zika is an arbovirus belonging to the same family as the dengue virus and is spread by the same vector, the *Aedes aegypti* mosquito.

It can also be spread by the tiger mosquito, *Aedes albopictus*, which is present in some regions in mainland France. Under the supervision of entomologist Anna-Bella Failloux, responsible for the Arboviruses and Insect Vectors Unit, the Institut Pasteur is currently conducting research

in Paris to assess the vectorial competence of *Aedes aegypti* and *Aedes albopictus*, and ascertain the role of these two species in the dynamics of the Zika epidemic. This work will help to better assess the risk of the virus being introduced to France.

More information: Antoine Enfissi et al. Zika virus genome from the Americas, *The Lancet* (2016). [DOI: 10.1016/S0140-6736\(16\)00003-9](https://doi.org/10.1016/S0140-6736(16)00003-9)

Provided by Institut Pasteur

Citation: First complete genome sequence of the Zika virus (2016, January 11) retrieved 4 July 2023 from <https://medicalxpress.com/news/2016-01-genome-sequence-zika-virus.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.